p#8

OIPE

RAW SEQUENCE LISTING   DATE: 07/25/2001
PATENT APPLICATION: **US/09/462,682**   TIME: 16:00:20

Input Set : **A:\Nih310-1.app**
Output Set: **N:\CRF3\07252001\I462682.raw**

ENTERED

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 3 <110> APPLICANT: FitzGerald, David J.
 4       The Government of the United States of America
 5       as represented by the Secretary,
 6       Department of Health and Human Services
 8 <120> TITLE OF INVENTION: Pseudomonas Exotoxin A-Like Chimeric Immunogens
10 <130> FILE REFERENCE: 015280-310100US
12 <140> CURRENT APPLICATION NUMBER: US 09/462,682
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C--> `13 <141> CURRENT FILING DATE: 2001-07-13`
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15 <150> PRIOR APPLICATION NUMBER: US 60/052,375
16 <151> PRIOR FILING DATE: 1997-07-11
18 <150> PRIOR APPLICATION NUMBER: WO PCT/US98/14341
19 <151> PRIOR FILING DATE: 1998-07-10
21 <160> NUMBER OF SEQ ID NOS: 13
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1839
27 <212> TYPE: DNA
28 <213> ORGANISM: Pseudomonas aeruginosa
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1839)
33 <223> OTHER INFORMATION: exotoxin A
35 <400> SEQUENCE: 1
36 gcc gaa gaa gct ttc gac ctc tgg aac gaa tgc gcc aaa gcc tgc gtg   48
37 Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
38  1               5                  10                  15
40 ctc gac ctc aag gac ggc gtg cgt tcc agc cgc atg agc gtc gac ccg   96
41 Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
42              20                  25                  30
44 gcc atc gcc gac acc aac ggc cag ggc gtg ctg cac tac tcc atg gtc  144
45 Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
46          35                  40                  45
48 ctg gag ggc ggc aac gac gcg ctc aag ctg gcc atc gac aac gcc ctc  192
49 Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
50      50                  55                  60
52 agc atc acc agc gac ggc ctg acc atc cgc ctc gaa ggc ggc gtc gag  240
53 Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
54  65                  70                  75                  80
56 ccg aac aag ccg gtg cgc tac agc tac acg cgc cag gcg cgc ggc agt  288
57 Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
58                  85                  90                  95
60 tgg tcg ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tcg aac  336
61 Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
62              100                 105                 110
64 atc aag gtg ttc atc cac gaa ctg aac gcc ggc aac cag ctc agc cac  384
65 Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
66          115                 120                 125
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 68 atg tcg ccg atc tac acc atc gag atg ggc gac gag ttg ctg gcg aag    432
 69 Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
 70     130                 135             140
 72 ctg gcg cgc gat gcc acc ttc ttc gtc agg gcg cac gag agc aac gag    480
 73 Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
 74 145                 150             155                 160
 76 atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg    528
 77 Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
 78                 165             170                 175
 80 gcc cag acc cag ccg cgc cgg gaa aag cgc tgg agc gaa tgg gcc agc    576
 81 Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
 82             180             185                 190
 84 ggc aag gtg ttg tgc ctg ctc gac ccg ctg gac ggg gtc tac aac tac    624
 85 Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
 86         195             200             205
 88 ctc gcc cag caa cgc tgc aac ctc gac gat acc tgg gaa ggc aag atc    672
 89 Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
 90     210             215             220
 92 tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac atc aaa    720
 93 Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
 94 225             230             235                 240
 96 ccc acg gtc atc agt cat cgc ctg cac ttt ccc gag ggc ggc agc ctg    768
 97 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
 98                 245             250                 255
100 gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc    816
101 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
102             260             265             270
104 acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag tgc ggc    864
105 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
106         275             280             285
108 tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg cgg ctg tcg    912
109 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
110     290             295             300
112 tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc ccc ggc    960
113 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
114 305                 310             315                 320
116 agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc   1008
117 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
118             325             330                 335
120 cgt ctg gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc gtc cgg   1056
121 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
122             340             345             350
124 cag ggc acc ggc aac gac gag gcc ggc gcg gcc aac gcc gac gtg gtg   1104
125 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
126         355             360             365
128 agc ctg acc tgc ccg gtc gcc gcc ggt gaa tgc gcg ggc ccg gcg gac   1152
129 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
130     370             375             380
132 agc ggc gac gcc ctg ctg gag cgc aac tat ccc act ggc gcg gag ttc   1200
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133 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe
134 385             390             395             400
136 ctc ggc gac ggc ggc gac gtc agc ttc agc acc cgc ggc acg cag aac   1248
137 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
138             405             410             415
140 tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag gag cgc   1296
141 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
142             420             425             430
144 ggc tat gtg ttc gtc ggc tac cac ggc acc ttc ctc gaa gcg gcg caa   1344
145 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
146         435             440             445
148 agc atc gtc ttc ggc ggg gtg cgc gcg cgc agc cag gac ctc gac gcg   1392
149 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
150     450             455             460
152 atc tgg cgc ggt ttc tat atc gcc ggc gat ccg gcg ctg gcc tac ggc   1440
153 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
154 465             470             475             480
156 tac gcc cag gac cag gaa ccc gac gca cgc ggc cgg atc cgc aac ggt   1488
157 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
158             485             490             495
160 gcc ctg ctg cgg gtc tat gtg ccg cgc tcg agc ctg ccg ggc ttc tac   1536
161 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
162             500             505             510
164 cgc acc agc ctg acc ctg gcc gcg ccg gag gcg gcg ggc gag gtc gaa   1584
165 Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
166         515             520             525
168 cgg ctg atc ggc cat ccg ctg ccg ctg cgc ctg gac gcc atc acc ggc   1632
169 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
170     530             535             540
172 ccc gag gag gaa ggc ggg cgc ctg gag acc att ctc ggc tgg ccg ctg   1680
173 Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
174 545             550             555             560
176 gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac ccg cgc   1728
177 Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
178             565             570             575
180 aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag   1776
181 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
182             580             585             590
184 gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa ccg ccg   1824
185 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
186         595             600             605
188 cgc gag gac ctg aag                                               1839
189 Arg Glu Asp Leu Lys
190     610
193 <210> SEQ ID NO: 2
194 <211> LENGTH: 613
195 <212> TYPE: PRT
196 <213> ORGANISM: Pseudomonas aeruginosa
198 <400> SEQUENCE: 2
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199 Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
200   1           5               10          15
202 Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
203          20              25              30
205 Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
206          35              40              45
208 Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
209      50              55              60
211 Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
212 65              70              75              80
214 Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
215              85              90              95
217 Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
218          100             105             110
220 Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
221          115             120             125
223 Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
224      130             135             140
226 Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
227 145             150             155             160
229 Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
230              165             170             175
232 Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
233              180             185             190
235 Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
236          195             200             205
238 Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
239      210             215             220
241 Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
242 225             230             235             240
244 Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
245              245             250             255
247 Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
248              260             265             270
250 Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
251          275             280             285
253 Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
254      290             295             300
256 Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
257 305             310             315             320
259 Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
260              325             330             335
262 Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
263              340             345             350
265 Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
266              355             360             365
268 Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
269      370             375             380
271 Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe
```

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```
272 385                    390                    395              .  400
274 Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
275             405                    410                    415
277 Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
278             420                    425                    430
280 Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
281     .       435                    440                    445
283 Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
284       450                    455              ·   460
286 Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
287 465                    470                    475                480
289 Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
290             485                    490                    495   ·    .
292 Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
293             500                    505                    510
295 Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
296         515                    520                    525
298 Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
299       530                    535                    540
301 Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
302 545                    550                    555                560
304 Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
305             565                    570                    575
307 Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
308             580                    585                    590
310 Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
311         595                    600                    605
313 Arg Glu Asp Leu Lys
314       610
318 <210> SEQ ID NO: 3
319 <211> LENGTH: 35
320 <212> TYPE: PRT
321 <213> ORGANISM: Human immunodeficiency virus type 1
323 <220> FEATURE:
324 <221> NAME/KEY: PEPTIDE
325 <222> LOCATION: (1)..(35)
326 <223> OTHER INFORMATION: V3 loop of MN strain of HIV-1
328 <400> SEQUENCE: 3
329 Cys Thr Arg Pro Asn Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro
330   1              5                    10                   15
332 Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr Ile Arg Gln
333             20                    25                    30
335 Ala His Cys
336           35
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 35
341 <212> TYPE: PRT
342 <213> ORGANISM: Human immunodeficiency virus type 1
344 <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 07/25/2001
PATENT APPLICATION: **US/09/462,682**   TIME: 16:00:21

Input Set : **A:\Nih310-1.app**
Output Set: **N:\CRF3\07252001\I462682.raw**

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date